Supplementary methods

GWAS data generation and quality control

ALSPAC children were genotyped using the Illumina HumanHap550 quad chip genotyping platforms. The resulting raw genome-wide data were subjected to standard quality control methods. Individuals were excluded on the basis of gender mismatches; minimal or excessive heterozygosity; disproportionate levels of individual missingness (>3%) and insufficient sample replication (IBD < 0.8). Population stratification was assessed by multidimensional scaling analysis and compared with Hapmap II (release 22) European descent (CEU), Han Chinese, Japanese and Yoruba reference populations; all individuals with non-European ancestry were removed. SNPs with a minor allele frequency of < 1%, a call rate of < 95% or evidence for violations of Hardy-Weinberg equilibrium (P < 5E-7) were removed. Cryptic relatedness was measured as proportion of identity by descent (IBD > 0.1). Related subjects that passed all other quality control thresholds were retained during subsequent phasing and imputation. 9,115 subjects and 500,527 SNPs passed these quality control filters.

ALSPAC mothers were genotyped using the Illumina human660W-quad array at Centre National de Génotypage (CNG) and genotypes were called with Illumina GenomeStudio. PLINK (v1.07) was used to carry out quality control measures on an initial set of 10,015 subjects and 557,124 directly genotyped SNPs. SNPs were removed if they displayed more than 5% missingness or a Hardy-Weinberg equilibrium P value of less than 1.0e-06. Additionally, SNPs with a minor allele frequency of less than 1% were removed. Samples were excluded if they displayed more than 5% missingness, had indeterminate X chromosome heterozygosity or extreme autosomal heterozygosity. Samples showing evidence of population stratification were identified by multidimensional scaling of genome-wide identity by state pairwise distances using the four HapMap populations as a reference, and then excluded. Cryptic relatedness was assessed using a IBD estimate of more than 0.125 which is expected to correspond to roughly 12.5% alleles shared IBD or a relatedness at the first cousin level. Related subjects that passed all other quality control thresholds were retained during subsequent phasing and imputation. 9,048 subjects and 526,688 SNPs passed these quality control filters.

After combining genotype data in the mothers and the children, SNPs with genotype missingness above 1% were removed due to poor quality (11,396 SNPs removed) and a further 321 subjects were removed due to potential ID mismatches. This resulted in a dataset of 17,842 subjects. Imputation of the target data was performed using Impute V2.2.2 against the 1000 genomes reference panel (Phase 1, Version 3) (all polymorphic SNPs excluding singletons), using all 2186 reference haplotypes (including non-Europeans).

This gave 8,237 eligible children and 8,196 eligible mothers with available genotype data after exclusion of related subjects using cryptic relatedness measures described previously.

PRSice

We used the PRSice software (http://prsice.info/) to generate polygenic scores for each trait within the ALSPAC genome-wide data. PRSice performs linkage disequilibrium clumping based on SNPs available in both GWAS and target datasets. We excluded SNPs with an R^2 of >0.1, which were within 250Kb of each other. SNPs located in the extended MHC region (chromosome 6 (26-33Mb)) were excluded. We used the following p-value thresholds to define polygenic scores: 0.0005, 0.005, 0.05, 0.1, 0.5. Analyses were performed separately in mothers and children using bestguess genotypes generated from the imputed data, filtered on a minor allele frequency >0.01 and imputation quality of >0.8.

Table S1. Timepoints of questionnaires and clinics included in participation phenotype

	Mother questionnaires	Mother clinics	Child based questionnaires	Child completed questionnaires	Child clinics
1	8-42 weeks gestation	17-18 years	4 weeks	65 months	7 years
2	12 weeks gestation		6 months	69 months	8 years
3	18 weeks gestation		15 months	73 months	9 years
4	32 weeks gestation		18 months	77 months	10 + years
5	8 weeks		24 months	81 months	11 + years
6	8 months		30 months	85 months	13 years
7	21 months		38 months	91 months	14 years
8	33 months		42 months	97 months	15 years
9	47 months		54 months	103 months	18 years
10	61 months		57 months	110 months	
11	85 months		65 months	115 months	
12	73 months		69 months	122 months	
13	97 months		77 months	128 months	
14	110 months		81 months	134 months	
15	122 months		91 months	140 months	
16	134 months		103 months	145 months	
17	145 months		103 months	157 months	
18	18 years +		115 months	157 months	
19	19 years +		128 months	166 months	
20			140 months	167 months	
21			157 months	169 months	
22			166 months	198 months	
23			198 months	18 years	
24			19 years +	20 years	

Table S2. Description of polygenic risk scores

Trait	Reference	Data available at:
Body mass index	Locke et al. (*1*)	http://portals.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium_data_files
Height	Wood et al. (*2*)	http://portals.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium_data_files
Smoking initiation	Furberg et al. (*3*)	https://www.med.unc.edu/pgc
Education	Okbay et al. (*4*)	https://www.thessgac.org/data
Sleep	Jones et al. (*5*)	http://www.t2diabetesgenes.org/data/
Morningness	Jones et al. (*5*)	http://www.t2diabetesgenes.org/data/
Age at Menarche	Perry et al. (*6*)	http://www.reprogen.org/data_download.html
Depression	Okbay et al. (*7*)	https://www.thessgac.org/data
Schizophrenia	Schizophrenia working group of Psychiatric Genomics Consortium (*8*)	https://www.med.unc.edu/pgc
ADHD	Psychiatric Genomics Consortium (PGC) and the Lundbeck Foundation Initiative for Integrative Psychiatric Research (iPSYCH) (*9*)	https://www.med.unc.edu/pgc
Bipolar	Cross-Disorder Group of the Psychiatric Genomics Consortium (*10*)	
Autism		
Agreeableness	De Moor et al. (*11*)	http://www.tweelingenregister.org/GPC/
Conscientiousness		
Extraversion		
Openness		
Neuroticism		
Alzheimer's Disease	Lambert et al. (*12*)	http://web.pasteur-lille.fr/en/recherche/u744/igap/igap_download.php

Table S3 Genomewide scores for traits generate in PRSice

Trait	Number of independent genomewide SNPs in original GWAS paper	Number in score generate using PRSice
Years of Education	74	64
BMI	77 (in Europeans)	72
Smoking initiation	1	1
Morningness	11 (in discovery sample which were replicated)	7
Sleep	3	2
Age at menarche	123	108
Alzheimer's	19 (in discovery sample which were replicated)	18
ADHD	12 (in full ADHD GWAS)	8
Depression	2	2
Schizophrenia	128	95
Height	697	535
Autism	1	1
Bipolar	4	4
Conscientiousness	1	1
Openness	2	1

Table S4 Dichomisation point for sensitivity analyses using continuous variables

Individual	Metric	Model	Dichotomisation point
Mother	Mother questionnaire	Logistic	12
	Total questionnaire		30
	Total participation		30
	Most recent clinic		NA
	Most recent questionnaire		NA
Child	Child questionnaire	Logistic	5
	Total questionnaire		30
	Total participation		30
	Child clinic		4
	Most recent clinic		NA
	Most recent questionnaire		NA

Table S5. Comparison of analysis sample with full sample.

	Mother		Child	
	Analysis sample (N=7,486)	**Full sample (N=13,793)**	**Analysis sample (N=7,508)**	**Full sample (N=13,953)**
	Mean (SD)	**Mean (SD)**	**Mean (SD)**	**Mean (SD)**
Total Participation	50.6 (23.8)	44.0 (25.5)	53.5 (22.0)	44.0 (25.4)
Total Questionnaire	45.0 (20.7)	39.5 (22.2)	47.4 (19.2)	39.4 (22.2)
Mother Questionnaire	14.0 (5.2)	12.7 (5.7)	-	-
Child Questionnaire	-	-	14.8 (8.0)	11.7 (8.8)
Child Clinic	-	-	5.7 (3.4)	4.2 (3.7)
	N (%)	**N (%)**	**N (%)**	**N (%)**
Mother attended most recent clinic	3,215 (43.0)	4,634 (33.6)	-	-
Mother completed most recent questionnaire	3,052 (40.8)	4,468 (32.4)	-	-
Child attended most recent clinic	-		3,538 (47.1)	4,878 (35.0)
Child completed most recent questionnaire	-		2,957 (39.4)	4,147 (29.7)

Table S6. Correlations between continuous participation phenotypes

	Child				Mother			
	Total	Total questionnaire	Child questionnaire	Child clinic		Total	Total questionnaire	Mother questionnaire
Total	1				Total	1		
Total questionnaire	0.9867	1			Total questionnaire	0.9877	1	
Child questionnaire	0.9505	0.9611	1		Mother questionnaire	0.9379	0.948	1
Child clinic	0.8093	0.7202	0.7193	1				

Correlation coefficients are Spearman's rank correlations

Table S7. Pearson's correlation coefficients between genetic risk scores generated at p<0.5 in the ALSPAC mothers (N=7,468)

	BMI	Morning	Sleep	Smoking	Education	Autism	Schiz	Dep	BPD	ADHD	Alzh	Agreeable	Consc	Extraversion	Neuroticism	Open	Height	Menarche
BMI	1																	
Morningness	0.0171	1																
Sleep	-0.0029	-0.0071	1															
Smoking	0.0386	-0.0073	-0.0126	1														
Education	-0.1332	-0.0383	0.0222	-0.0499	1													
Autism	-0.014	-0.0108	-0.0073	0.002	0.0418	1												
Schizophrenia	-0.0041	-0.0207	0.0199	0.0935	0.0426	0.0128	1											
Depression	0.0518	-0.0725	-0.0502	0.0437	-0.1136	0.0025	0.0518	1										
Bipolar disorder	-0.005	-0.0275	0.0073	0.0128	0.0446	0.0132	0.1716	0.0476	1									
ADHD	-0.0066	-0.0047	0.0046	0.0282	-0.0312	0.0253	0.0325	0.0148	0.0334	1								
Alzheimer's disease	0.0106	0.0143	-0.0069	-0.0037	-0.0309	-0.0211	0.0257	0.0024	0.0061	-0.0029	1							
Agreeableness	-0.0208	-0.0226	-0.0007	-0.0277	0.0465	0.0094	-0.0105	-0.0272	0.0101	0.0035	0.0031	1						
Conscientiousness	0.0096	0.0353	-0.0058	-0.0698	-0.0101	-0.0156	-0.0292	-0.0109	-0.0301	-0.0074	0.0139	0.2143	1					
Extraversion	0.02	0.0053	0.0094	0.0233	0.0075	-0.002	0.0345	-0.0149	0.0004	0.0083	0.0032	0.2388	0.3295	1				
Neuroticism	-0.0191	-0.0025	0.0018	-0.0027	-0.0173	0.0021	-0.0001	0.0252	-0.0057	-0.0052	-0.012	-0.2269	-0.2966	-0.4009	1			
Openness	0.0012	-0.0175	0.0108	0.0226	0.0577	0.0325	0.0527	0.0013	0.0138	0.0048	-0.012	0.071	-0.0377	0.1542	-0.0859	1		
Height	-0.109	0.0099	-0.0033	-0.1056	0.0517	-0.0038	-0.0952	-0.012	-0.0298	-0.0168	-0.0097	0.0091	0.0406	-0.0208	-0.0501	-0.0321	1	
Age at menarche	-0.1544	0.0014	0.0232	0.0219	0.0363	0.021	0.0308	-0.0229	0.0051	-0.0182	0.0049	0.0134	0.0084	0.0175	-0.029	-0.0257	0.0743	1

Table S8. Pearson's correlation coefficients between genetic risk scores generated at p<0.0005 in the ALSPAC mothers (N=7,468)

	BMI	Morning	Sleep	Smoking	Education	Autism	Schiz	Dep	BPD	ADHD	Alzh	Agreeable	Consc	Extraversion	Neuroticism	Open	Height	Menarche
BMI	1																	
Morningness	-0.0005	1																
Sleep	0.0134	-0.0146	1															
Smoking	-0.0005	0.0022	-0.0043	1														
Education	-0.0784	-0.023	0.0036	-0.0097	1													
Autism	0	-0.0447	-0.0316	0.0207	0.0437	1												
Schizophrenia	0.0138	-0.0121	0.0737	0.0199	0.0392	-0.0228	1											
Depression	-0.0077	-0.0162	-0.0299	0.0144	-0.0363	0.0224	0.0236	1										
Bipolar disorder	0.0005	-0.0144	-0.002	0.005	0.0482	-0.0047	0.0897	0.0204	1									
ADHD	-0.015	-0.004	0.0033	0.0077	-0.0075	-0.0088	0.006	0.0004	0.0149	1								
Alzheimer's disease	-0.0144	0.0141	-0.0005	-0.0113	-0.0196	-0.0098	0.0144	-0.0096	-0.0012	0.0048	1							
Agreeableness	0.0215	-0.0119	-0.0152	-0.0125	0.0058	-0.0072	0.0091	-0.0127	-0.0039	0.0006	-0.0085	1						
Conscientiousness	0.0243	-0.0009	0.006	0.0086	-0.0142	0.0015	0.0043	0.0023	-0.0059	-0.0083	-0.0009	0.0118	1					
Extraversion	0.0098	-0.0027	-0.002	-0.0158	-0.0016	-0.0057	0.0095	0.0083	0.0016	0.001	0.009	0.0116	0.049	1				
Neuroticism	-0.0197	0.0037	-0.0014	0.0116	-0.0137	0.0122	-0.0032	0.0032	-0.0008	0.0011	-0.014	-0.0103	-0.0456	-0.0556	1			
Openness	0.0122	-0.0045	-0.0234	-0.0175	0.0389	-0.0044	0.0169	-0.0119	-0.009	-0.0021	-0.0023	0.0023	-0.0181	-0.008	-0.0025	1		
Height	-0.043	-0.0074	-0.019	0.0015	0.0589	0.0162	-0.0235	0.0004	0.0079	0.0238	0.023	-0.0011	-0.0197	0.008	-0.0102	0.0121	1	
Age at menarche	-0.1074	-0.0049	-0.005	0.0108	-0.0234	-0.023	-0.0119	-0.008	0.0123	-0.0211	0.0133	-0.0042	-0.0153	0.0116	0.0001	0.0104	0.0365	1

Table S9. Pearson's correlation coefficients between genetic risk scores generated at p<0.5 in the ALSPAC children (N=7,508)

	BMI	Morning	Sleep	Smoking	Education	Autism	Schiz	Dep	BPD	ADHD	Alzh	Agreeable	Consc	Extraversion	Neuroticism	Open	Height
BMI	1																
Morningness	0.0404	1															
Sleep	0.0015	-0.0012	1														
Smoking	0.0412	-0.0002	-0.0028	1													
Education	-0.1207	-0.0362	0.0421	-0.0524	1												
Autism	-0.007	0.007	0.0125	0.02	0.0541	1											
Schizophrenia	-0.0072	0.0031	0.0385	0.0651	0.0374	0.0068	1										
Depression	0.0441	-0.0614	-0.0657	0.0634	-0.1184	0.0235	0.0225	1									
Bipolar disorder	-0.0204	-0.0263	0.021	0.0125	0.055	-0.0033	0.1616	0.0165	1								
ADHD	-0.0006	0.0072	0.0047	0.0316	-0.0196	0.01	0.0155	-0.0029	0.028	1							
Alzheimer's disease	0.0116	0.0143	0.0064	0.012	-0.0367	-0.0041	0.0211	0.0006	0.0254	-0.0187	1						
Agreeableness	-0.0194	0.0167	0.0088	-0.0159	0.0403	-0.0069	-0.0186	-0.031	0.0243	-0.0339	0.0097	1					
Conscientiousness	0.0035	0.0051	-0.0028	-0.0447	-0.0079	-0.0101	-0.0208	-0.0042	-0.012	-0.0275	0.0211	0.2321	1				
Extraversion	0.0117	0.01	0.0031	0.0326	0.0146	-0.0012	0.0201	-0.0113	0.014	0.0062	0.0343	0.2165	0.3293	1			
Neuroticism	0.0009	0.0103	-0.0174	-0.0158	-0.0245	0.0048	0.0075	0.0282	-0.0182	-0.005	-0.0026	-0.2218	-0.283	-0.3859	1		
Openness	0.0192	-0.0045	0.0017	0.0429	0.0693	0.0238	0.0398	-0.0034	0.0175	0.0218	-0.0151	0.0734	-0.052	0.1504	-0.076	1	
Height	-0.1182	-0.0154	0.0032	-0.0924	0.036	0.0051	-0.0713	-0.0342	-0.0299	-0.0237	-0.0153	0.0123	0.0452	-0.0095	-0.0862	-0.077	1

Correlations with age at menarche in females (N=3,639)

	BMI	Morning	Sleep	Smoking	Education	Autism	Schiz	Dep	BPD	ADHD	Alzh	Agreeable	Consc	Extraversion	Neuroticism	Open	Height
Menarche (0.05)	-0.1736	-0.0088	0.0117	0.0171	0.0249	0.0067	0.0162	-0.0373	-0.0013	-0.0077	0.0185	-0.0146	0.0187	-0.005	0.0124	-0.042	0.0745

Table S10. Pearson's correlation coefficients between genetic risk scores generated at p<0.0005 in the ALSPAC children (N=7,508)

	BMI	Morning	Sleep	Smoking	Education	Autism	Schiz	Dep	BPD	ADHD	Alzh	Agreeable	Consc	Extraversion	Neuroticism	Open	Height
BMI	1																
Morningness	0.0108	1															
Sleep	0.0112	0.011	1														
Smoking	-0.005	-0.0016	0.0151	1													
Education	-0.0491	-0.0081	0.0254	-0.0297	1												
Autism	-0.0208	-0.0194	-0.0635	-0.008	0.0349	1											
Schizophrenia	0.0119	0.0007	0.0698	0.0365	0.0181	-0.0225	1										
Depression	-0.0067	-0.0325	-0.0444	-0.0017	-0.0306	0.027	0.0208	1									
Bipolar disorder	-0.0122	-0.0043	-0.0055	0.0126	0.0247	0.0014	0.1024	-0.003	1								
ADHD	-0.0035	-0.0003	0.015	-0.0047	-0.0008	-0.0115	-0.0085	-0.0041	-0.0034	1							
Alzheimer's disease	0.0008	0.0027	-0.0107	0.0027	-0.0181	-0.0026	0.0105	-0.0088	-0.0034	0.0008	1						
Agreeableness	-0.0071	-0.0074	-0.0031	-0.0097	0.0195	-0.0113	-0.0099	-0.0057	-0.0006	-0.0111	0.0078	1					
Conscientiousness	0.0054	0.009	0.0095	-0.0026	-0.0024	-0.0126	-0.0077	-0.0101	-0.0035	-0.0226	0.0083	0.0389	1				
Extraversion	0.0143	0.0024	0.0097	0.013	-0.0156	0.0019	0.0146	-0.0071	-0.0226	0.0037	0.0015	0.0284	0.0489	1			
Neuroticism	-0.028	-0.0372	-0.002	-0.0065	-0.0076	0.0089	-0.0008	0.0137	0.0057	0.0175	-0.0325	-0.009	-0.057	-0.0679	1		
Openness	0.0035	-0.0184	-0.0143	-0.008	0.0257	0.0005	0.0253	-0.021	0.004	-0.0173	0.0184	-0.0191	0.0064	0.0067	0.0125	1	
Height	-0.0402	-0.0222	-0.0055	-0.0163	0.0589	0.0101	-0.0306	-0.0293	0.0046	0.0257	0.0134	0	-0.023	0.0321	-0.0123	-0.02	1

Correlations with age at menarche in females (N=3,639)

	BMI	Morning	Sleep	Smoking	Education	Autism	Schiz	Dep	BPD	ADHD	Alzh	Agreeable	Consc	Extraversion	Neuroticism	Open	Height
Menarche (0.0005)	-0.1304	-0.0086	-0.0005	0.0091	-0.023	-0.0029	0.0323	-0.0233	0.0412	-0.0082	-0.0013	-0.0289	0.0085	-0.0023	0.0022	-0.029	0.038

Table S11. Genomewide significant associations with total participation in mothers

SNP	CHR	BP	A1	A2	Beta	SE	P	A1_freq	info
rs10626545	7	51999752	TCA	T	10.97	1.81	1.50E-09	0.987	0.94
rs406001	7	52006415	C	T	10.86	1.80	1.67E-09	0.988	1.00
rs10234957	7	52011171	A	G	10.83	1.81	2.12E-09	0.988	1.00
rs10265236	7	52011178	T	C	10.83	1.81	2.12E-09	0.988	1.00
rs392252	7	52039815	G	A	10.84	1.81	2.15E-09	0.988	1.00
rs413648	7	52013580	G	T	10.81	1.81	2.23E-09	0.988	1.00
rs403531	7	52007845	G	A	10.81	1.81	2.23E-09	0.988	1.00
rs616199	7	52014884	C	A	10.81	1.81	2.23E-09	0.988	1.00
rs428360	7	52015414	A	T	10.81	1.81	2.23E-09	0.988	1.00
rs410473	7	52015969	A	G	10.81	1.81	2.24E-09	0.988	1.00
rs382903	7	52033199	A	G	10.81	1.81	2.24E-09	0.988	1.00
rs377851	7	52031652	T	A	10.81	1.81	2.24E-09	0.988	1.00
rs364752	7	52021977	T	C	10.81	1.81	2.25E-09	0.988	1.00
rs417388	7	52029191	T	C	10.81	1.81	2.25E-09	0.988	1.00
rs454526	7	52030332	C	A	10.81	1.81	2.25E-09	0.988	1.00
rs411093	7	52007969	C	T	10.81	1.81	2.26E-09	0.988	1.00
rs411481	7	52008508	G	A	10.81	1.81	2.26E-09	0.988	1.00
rs402450	7	52008755	A	G	10.81	1.81	2.26E-09	0.988	1.00
rs455017	7	52002774	C	T	10.86	1.82	2.27E-09	0.988	0.99
rs396471	7	52005401	G	T	10.84	1.81	2.28E-09	0.988	1.00
rs590600	7	52004473	A	T	10.85	1.81	2.30E-09	0.988	0.99
rs384551	7	52001102	A	G	10.86	1.82	2.31E-09	0.988	0.99
rs409776	7	52001673	T	G	10.86	1.82	2.31E-09	0.988	0.99
rs408595	7	52000754	C	T	10.86	1.82	2.31E-09	0.988	0.99
rs608826	7	52000958	G	A	10.86	1.82	2.32E-09	0.988	0.99
rs438867	7	51999538	T	C	10.87	1.82	2.32E-09	0.988	0.99
rs382727	7	51998920	C	T	10.87	1.82	2.33E-09	0.988	0.99
rs379235	7	51998152	A	T	10.87	1.82	2.33E-09	0.988	0.99
rs426522	7	51997533	T	C	10.87	1.82	2.34E-09	0.988	0.99
rs454404	7	51996191	C	T	10.99	1.84	2.46E-09	0.989	0.98
rs452777	7	51995163	C	T	10.99	1.84	2.50E-09	0.989	0.98
rs10480946	7	52009321	C	T	10.70	1.80	2.64E-09	0.988	0.99
rs6971505	7	52009980	A	T	10.90	1.86	5.14E-09	0.989	1.00
rs400204	7	52014571	A	G	10.90	1.86	5.15E-09	0.989	1.00
rs424283	7	52023670	A	G	10.90	1.86	5.16E-09	0.989	1.00
rs201492164	7	51999316	T	TTG	10.44	1.81	8.08E-09	0.988	0.96
rs664926	7	52016205	A	T	10.02	1.74	8.17E-09	0.987	1.00
rs647653	7	52042739	C	T	9.67	1.73	2.07E-08	0.987	0.99
rs428955	7	52042976	T	A	9.54	1.73	3.24E-08	0.987	0.97
rs201423711	7	51999664	AT	A	8.77	1.59	3.52E-08	0.981	0.81
rs11405039	7	51999666	TG	T	8.77	1.59	3.52E-08	0.981	0.81

Table S12. Genomewide significant associations with total questionnaire in mothers

SNP	CHR	BP	A1	A2	Beta	SE	P	A1_freq	info
rs10626545	7	51999752	TCA	T	9.65	1.57	8.55E-10	0.987	0.94
rs406001	7	52006415	C	T	9.53	1.56	1.05E-09	0.988	1.00
rs392252	7	52039815	G	A	9.55	1.57	1.22E-09	0.988	1.00
rs10234957	7	52011171	A	G	9.51	1.56	1.27E-09	0.988	1.00
rs10265236	7	52011178	T	C	9.51	1.56	1.27E-09	0.988	1.00
rs382903	7	52033199	A	G	9.50	1.57	1.34E-09	0.988	1.00
rs413648	7	52013580	G	T	9.50	1.57	1.34E-09	0.988	1.00
rs377851	7	52031652	T	A	9.50	1.57	1.35E-09	0.988	1.00
rs403531	7	52007845	G	A	9.50	1.57	1.35E-09	0.988	1.00
rs616199	7	52014884	C	A	9.50	1.57	1.35E-09	0.988	1.00
rs428360	7	52015414	A	T	9.50	1.57	1.35E-09	0.988	1.00
rs410473	7	52015969	A	G	9.50	1.57	1.35E-09	0.988	1.00
rs364752	7	52021977	T	C	9.50	1.57	1.36E-09	0.988	1.00
rs417388	7	52029191	T	C	9.50	1.57	1.36E-09	0.988	1.00
rs454526	7	52030332	C	A	9.50	1.57	1.36E-09	0.988	1.00
rs455017	7	52002774	C	T	9.55	1.57	1.36E-09	0.988	0.99
rs411093	7	52007969	C	T	9.50	1.57	1.36E-09	0.988	1.00
rs411481	7	52008508	G	A	9.50	1.57	1.36E-09	0.988	1.00
rs402450	7	52008755	A	G	9.50	1.57	1.36E-09	0.988	1.00
rs396471	7	52005401	G	T	9.53	1.57	1.37E-09	0.988	1.00
rs590600	7	52004473	A	T	9.54	1.57	1.38E-09	0.988	0.99
rs384551	7	52001102	A	G	9.55	1.58	1.38E-09	0.988	0.99
rs409776	7	52001673	T	G	9.55	1.57	1.38E-09	0.988	0.99
rs408595	7	52000754	C	T	9.55	1.58	1.38E-09	0.988	0.99
rs608826	7	52000958	G	A	9.55	1.58	1.39E-09	0.988	0.99
rs10480946	7	52009321	C	T	9.44	1.56	1.39E-09	0.988	0.99
rs438867	7	51999538	T	C	9.55	1.58	1.39E-09	0.988	0.99
rs382727	7	51998920	C	T	9.55	1.58	1.39E-09	0.988	0.99
rs379235	7	51998152	A	T	9.56	1.58	1.39E-09	0.988	0.99
rs426522	7	51997533	T	C	9.56	1.58	1.39E-09	0.988	0.99
rs454404	7	51996191	C	T	9.67	1.60	1.43E-09	0.989	0.98
rs452777	7	51995163	C	T	9.67	1.60	1.46E-09	0.989	0.98
rs6971505	7	52009980	A	T	9.71	1.62	1.99E-09	0.989	1.00
rs400204	7	52014571	A	G	9.71	1.62	1.99E-09	0.989	1.00
rs424283	7	52023670	A	G	9.71	1.62	2.00E-09	0.989	1.00
rs201492164	7	51999316	T	TTG	9.18	1.57	4.96E-09	0.988	0.96
rs664926	7	52016205	A	T	8.77	1.51	5.90E-09	0.987	1.00
rs647653	7	52042739	C	T	8.53	1.50	1.18E-08	0.987	0.99
rs428955	7	52042976	T	A	8.42	1.50	1.82E-08	0.987	0.97
rs201423711	7	51999664	AT	A	7.76	1.38	1.87E-08	0.981	0.81
rs11405039	7	51999666	TG	T	7.76	1.38	1.87E-08	0.981	0.81

Table S13. Genomewide significant associations with mother questionnaire in mothers

SNP	CHR	BP	A1	A2	Beta	SE	P	A1_freq	info
rs406001	7	52006415	C	T	2.27	0.39	8.27E-09	0.988	1.00
rs392252	7	52039815	G	A	2.27	0.40	9.84E-09	0.988	1.00
rs10234957	7	52011171	A	G	2.26	0.39	9.92E-09	0.988	1.00
rs10265236	7	52011178	T	C	2.26	0.39	9.92E-09	0.988	1.00
rs413648	7	52013580	G	T	2.26	0.39	1.07E-08	0.988	1.00
rs382903	7	52033199	A	G	2.26	0.39	1.07E-08	0.988	1.00
rs403531	7	52007845	G	A	2.26	0.39	1.07E-08	0.988	1.00
rs616199	7	52014884	C	A	2.26	0.39	1.07E-08	0.988	1.00
rs377851	7	52031652	T	A	2.26	0.39	1.07E-08	0.988	1.00
rs428360	7	52015414	A	T	2.26	0.39	1.07E-08	0.988	1.00
rs410473	7	52015969	A	G	2.26	0.39	1.07E-08	0.988	1.00
rs364752	7	52021977	T	C	2.26	0.39	1.08E-08	0.988	1.00
rs417388	7	52029191	T	C	2.26	0.39	1.08E-08	0.988	1.00
rs454526	7	52030332	C	A	2.26	0.39	1.08E-08	0.988	1.00
rs411093	7	52007969	C	T	2.26	0.39	1.08E-08	0.988	1.00
rs411481	7	52008508	G	A	2.26	0.39	1.08E-08	0.988	1.00
rs402450	7	52008755	A	G	2.26	0.39	1.08E-08	0.988	1.00
rs10480946	7	52009321	C	T	2.25	0.39	1.09E-08	0.988	0.99
rs455017	7	52002774	C	T	2.27	0.40	1.09E-08	0.988	0.99
rs396471	7	52005401	G	T	2.27	0.40	1.09E-08	0.988	1.00
rs590600	7	52004473	A	T	2.27	0.40	1.10E-08	0.988	0.99
rs384551	7	52001102	A	G	2.27	0.40	1.11E-08	0.988	0.99
rs408595	7	52000754	C	T	2.27	0.40	1.11E-08	0.988	0.99
rs409776	7	52001673	T	G	2.27	0.40	1.11E-08	0.988	0.99
rs608826	7	52000958	G	A	2.27	0.40	1.11E-08	0.988	0.99
rs438867	7	51999538	T	C	2.27	0.40	1.11E-08	0.988	0.99
rs382727	7	51998920	C	T	2.27	0.40	1.12E-08	0.988	0.99
rs379235	7	51998152	A	T	2.27	0.40	1.12E-08	0.988	0.99
rs426522	7	51997533	T	C	2.27	0.40	1.12E-08	0.988	0.99
rs10626545	7	51999752	TCA	T	2.26	0.40	1.12E-08	0.987	0.94
rs454404	7	51996191	C	T	2.30	0.40	1.18E-08	0.989	0.98
rs452777	7	51995163	C	T	2.30	0.40	1.20E-08	0.989	0.98
rs6971505	7	52009980	A	T	2.32	0.41	1.33E-08	0.989	1.00
rs400204	7	52014571	A	G	2.32	0.41	1.34E-08	0.989	1.00
rs424283	7	52023670	A	G	2.32	0.41	1.34E-08	0.989	1.00
rs201492164	7	51999316	T	TTG	2.18	0.40	3.63E-08	0.988	0.96
rs664926	7	52016205	A	T	2.07	0.38	4.79E-08	0.987	1.00

Table S14. Genomewide significant associations with total participation in children

SNP	CHR	BP	A1	A2	Beta	SE	P	A1_freq	info
rs28631073	14	96726466	G	A	-3.20	0.57	2.27E-08	0.11	1.00
rs10143977	14	96726883	G	T	-3.19	0.57	2.35E-08	0.11	1.00
rs10134118	14	96726986	T	C	-3.18	0.57	2.85E-08	0.11	1.00
rs11622768	14	96727554	T	C	-3.17	0.57	3.12E-08	0.11	1.00
rs10137303	14	96728002	G	A	-3.15	0.57	3.52E-08	0.11	1.00
rs10147171	14	96727874	C	T	-3.14	0.57	4.09E-08	0.11	1.00
rs4905475	14	96721850	C	G	-3.16	0.58	4.17E-08	0.11	0.99

Table S15. Genomewide significant associations with total questionnaire in children

SNP	CHR	BP	A1	A2	Beta	SE	P	A1_freq	info
rs28631073	14	96726466	G	A	-2.83	0.50	1.53E-08	0.11	1.00
rs10143977	14	96726883	G	T	-2.82	0.50	1.59E-08	0.11	1.00
rs10134118	14	96726986	T	C	-2.81	0.50	1.96E-08	0.11	1.00
rs11622768	14	96727554	T	C	-2.80	0.50	2.14E-08	0.11	1.00
rs10137303	14	96728002	G	A	-2.78	0.50	2.48E-08	0.11	1.00
rs4905475	14	96721850	C	G	-2.79	0.50	2.88E-08	0.11	0.99
rs10147171	14	96727874	C	T	-2.77	0.50	2.93E-08	0.11	1.00
rs11628515	14	96728111	A	T	-2.76	0.50	3.79E-08	0.11	1.00
rs45528931	14	96729885	A	G	-2.74	0.50	4.78E-08	0.11	0.99

Table S16. Genomewide significant associations with child questionnaire in children

SNP	CHR	BP	A1	A2	Beta	SE	P	A1_freq	info
rs28631073	14	96726466	G	A	-1.18	0.21	1.29E-08	0.11	1.00
rs10143977	14	96726883	G	T	-1.18	0.21	1.33E-08	0.11	1.00
rs10134118	14	96726986	T	C	-1.17	0.21	1.79E-08	0.11	1.00
rs11622768	14	96727554	T	C	-1.16	0.21	2.02E-08	0.11	1.00
rs10137303	14	96728002	G	A	-1.16	0.21	2.13E-08	0.11	1.00
rs10147171	14	96727874	C	T	-1.15	0.21	2.69E-08	0.11	1.00
rs4905475	14	96721850	C	G	-1.16	0.21	2.71E-08	0.11	0.99
rs11628515	14	96728111	A	T	-1.14	0.21	3.71E-08	0.11	1.00

Table S17. Genomewide significant associations with child clinic in children

SNP	CHR	BP	A1	A2	Beta	SE	P	A1_freq	info
rs1336852	1	191752825	G	A	-0.59	0.11	3.15E-08	0.07	0.98
rs74626786	1	191759598	G	C	-0.59	0.11	3.32E-08	0.07	0.98

Table S17. SNP-based heritability estimates from GCTA

	H^2	Standard error	P-value
Mother			
Total participation	0.271	0.045	7.00E-11
Total questionnaire	0.267	0.045	1.53E-19
Mother questionnaire	0.238	0.044	8.59E-09
Mother last clinic	0.225	0.045	9.70E-08
Mother last questionnaire	0.203	0.045	1.46E-06
Child			
Total participation	0.301	0.045	6.05E-13
Total questionnaire	0.287	0.045	7.03E-12
Child questionnaire	0.319	0.045	6.06E-14
Child clinic	0.249	0.044	9.10E-10
Child last clinic	0.249	0.045	4.00E-09
Child last questionnaire	0.178	0.045	2.52E-05

Adjusted for the first 10 genetic principal components.

Figure S1. Flowchart of ALSPAC mothers included in analysis

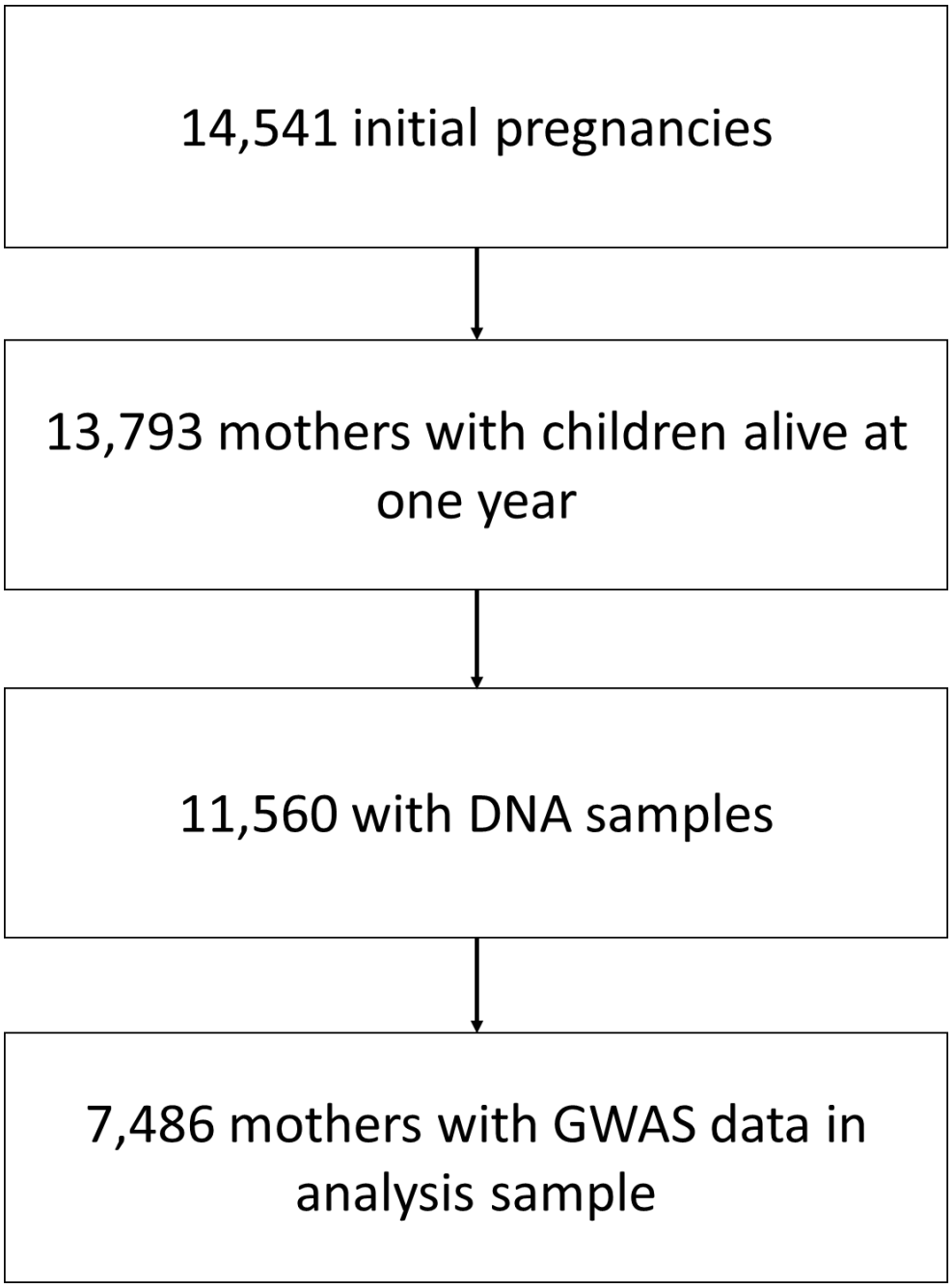


Figure S2. Flowchart of ALSPAC children included in analysis

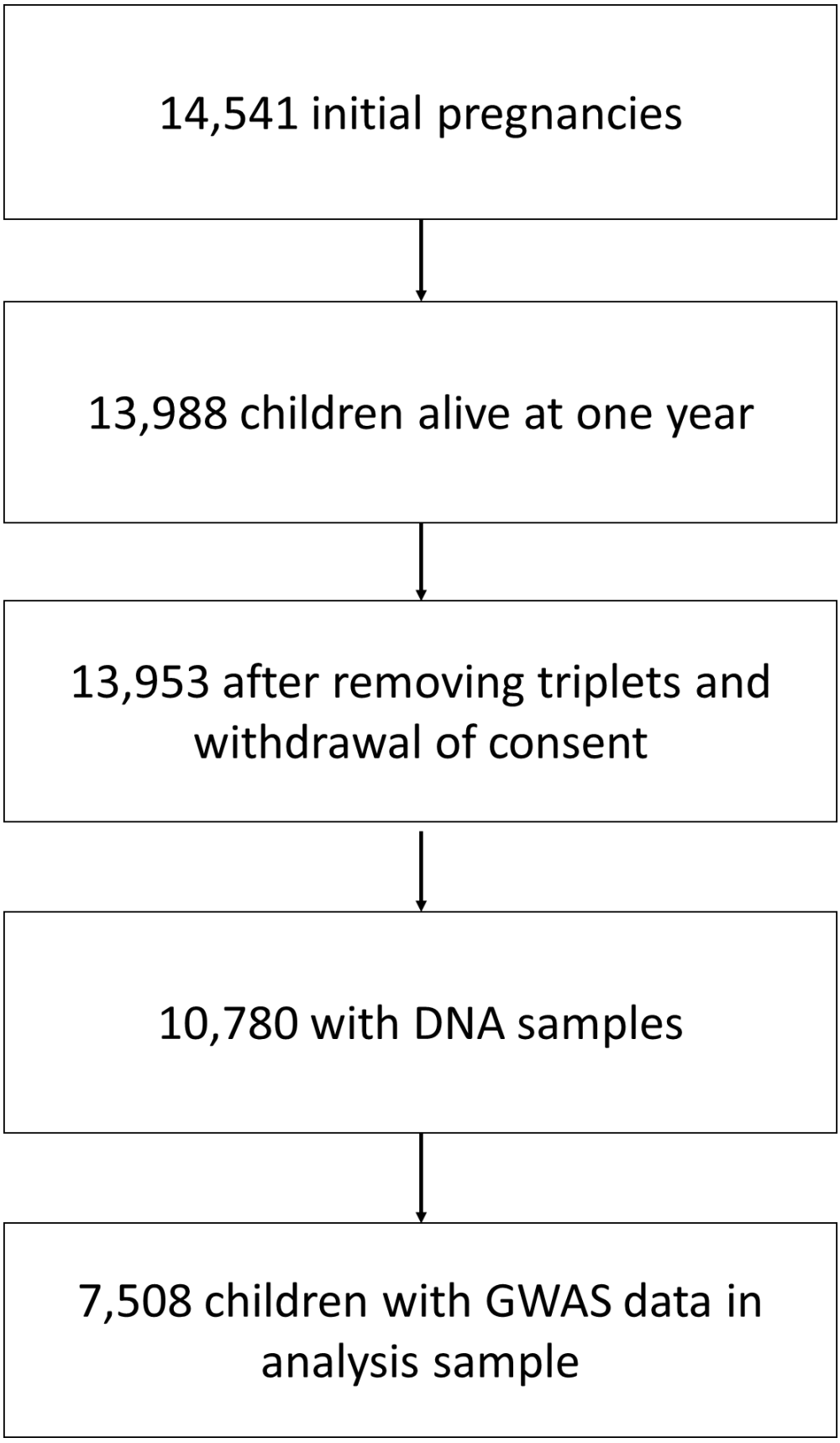
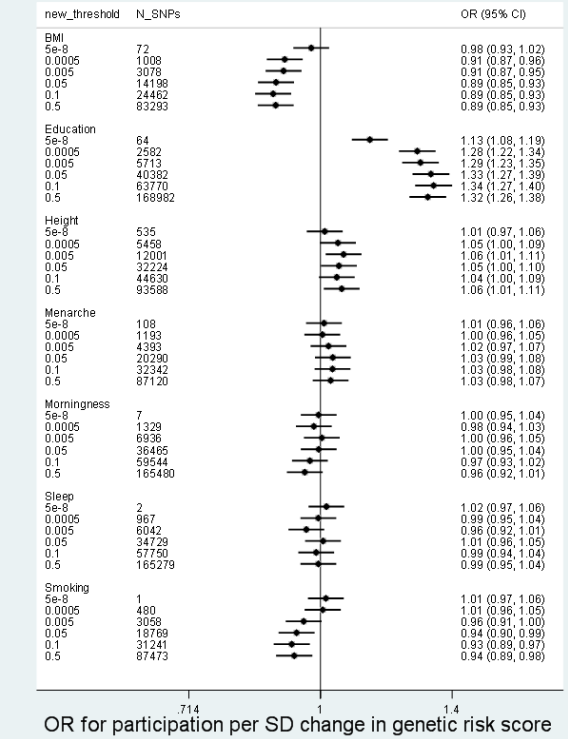
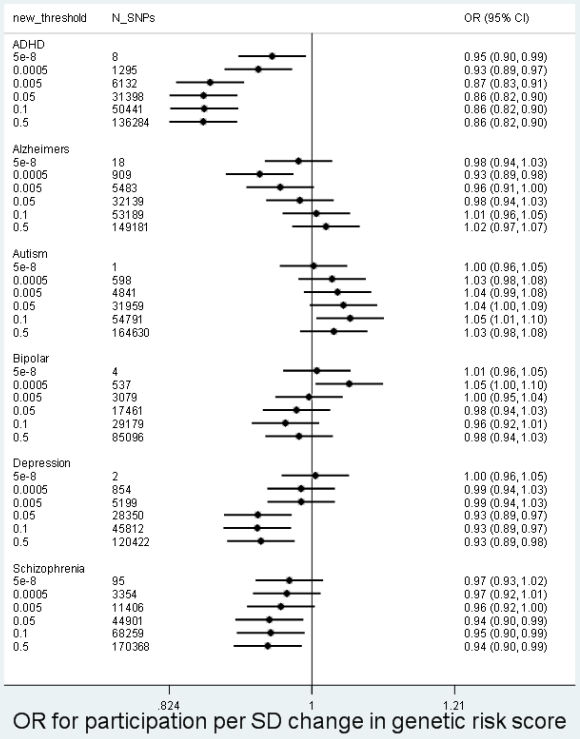


Figure S3. Associations between polygenic risk scores and attendance at most recent clinic in ALSPAC mothers (N=7,468)





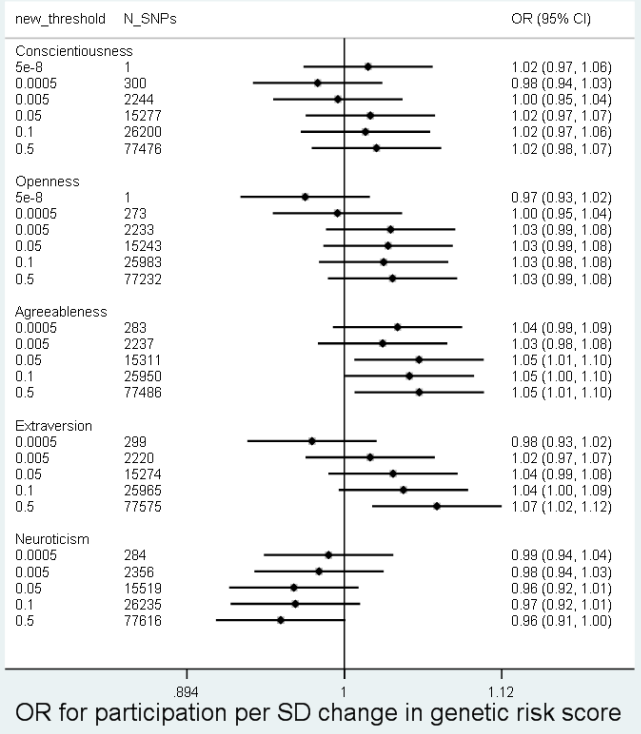
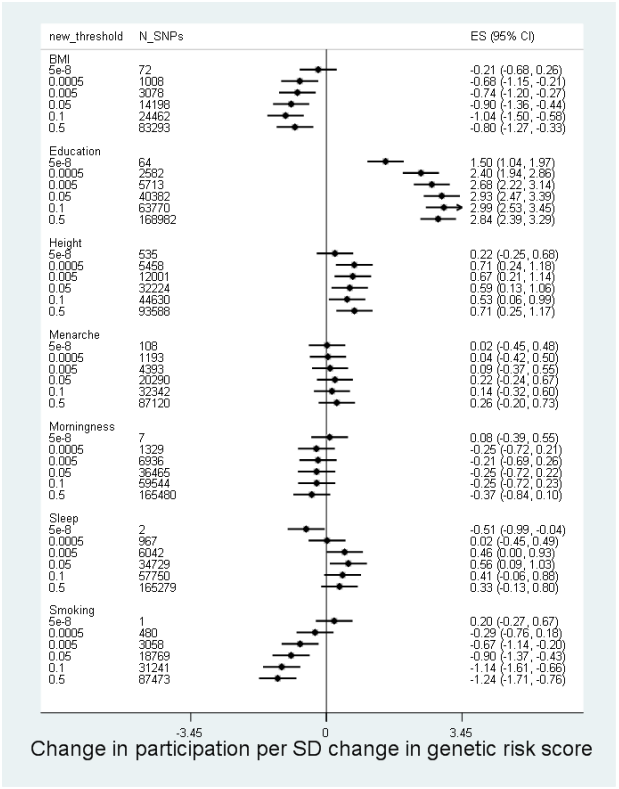
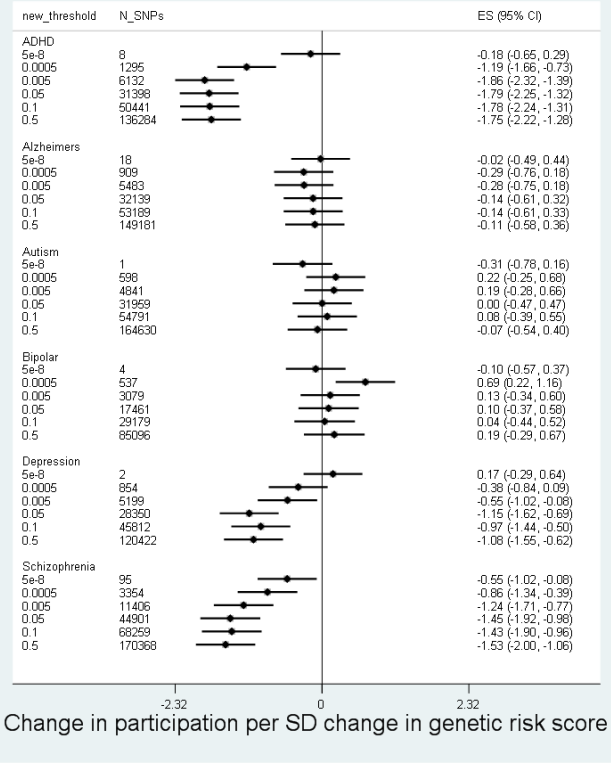


Figure S4. Associations between polygenic risk scores and total questionnaire completion in the mothers (N=7,468)





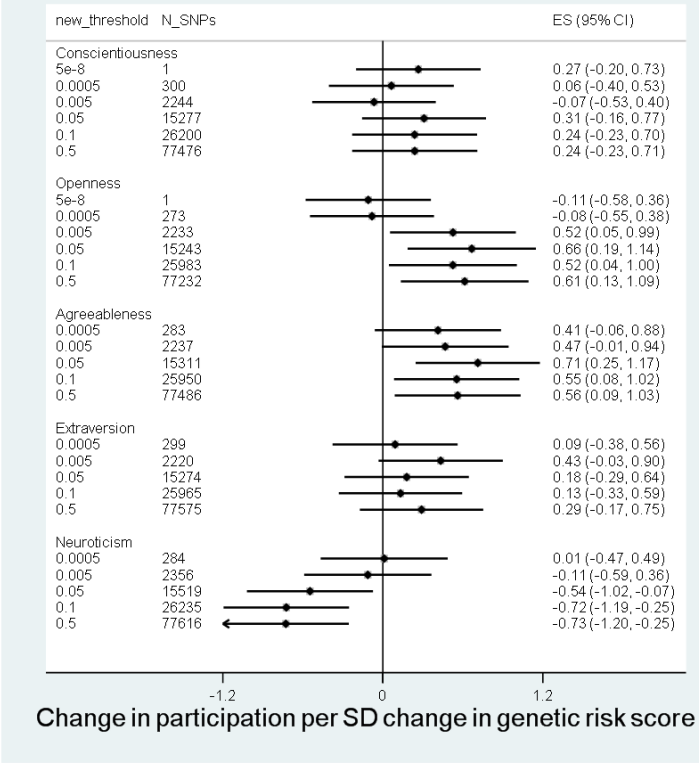


Figure S5. Associations between polygenic risk scores and mother questionnaires (N=7,468)

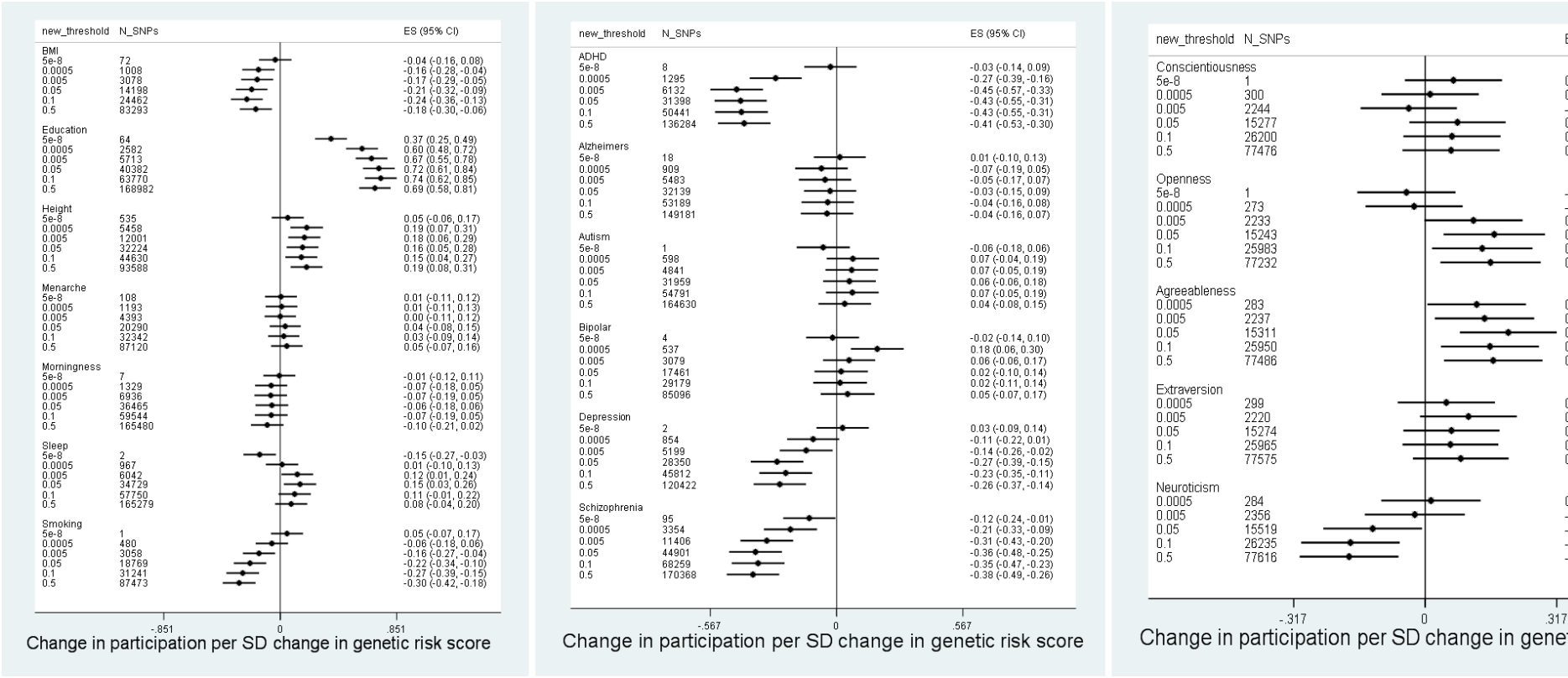
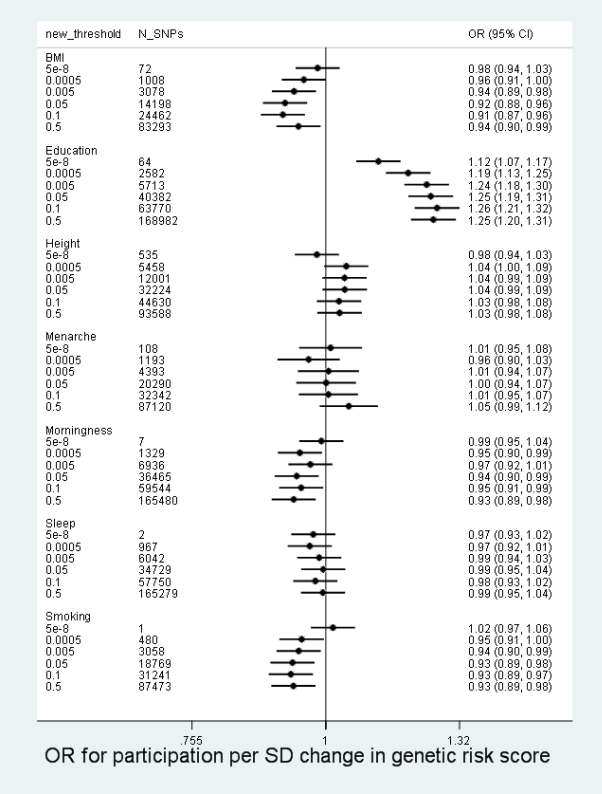
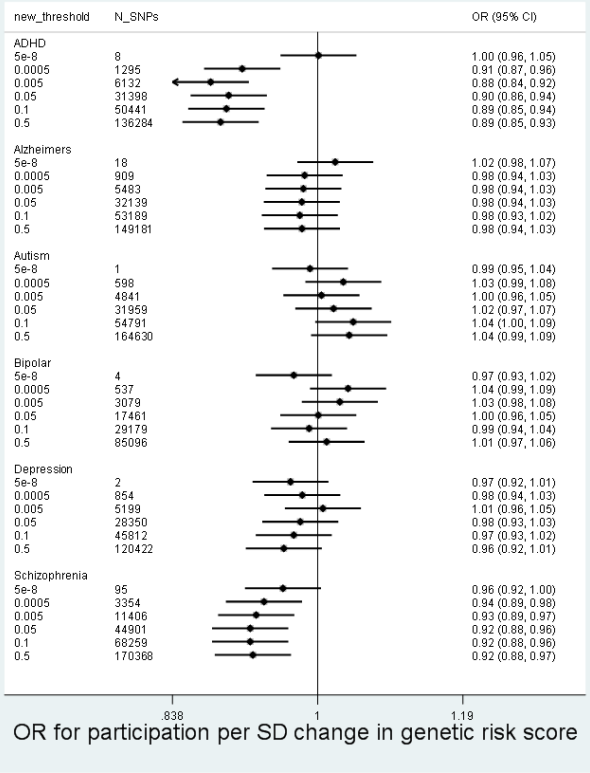
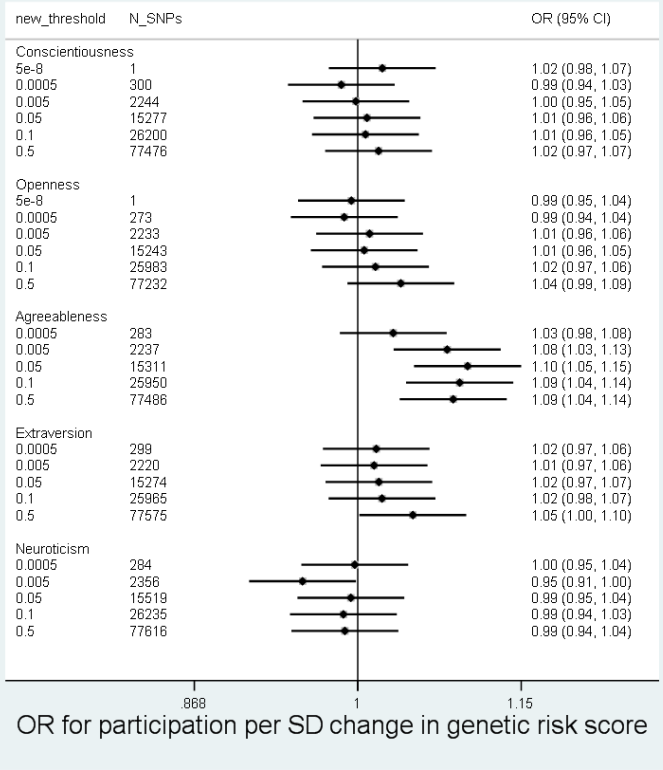


Figure S6. Associations between polygenic risk scores and attendance at most recent clinic in ALSPAC children (N=7,508)

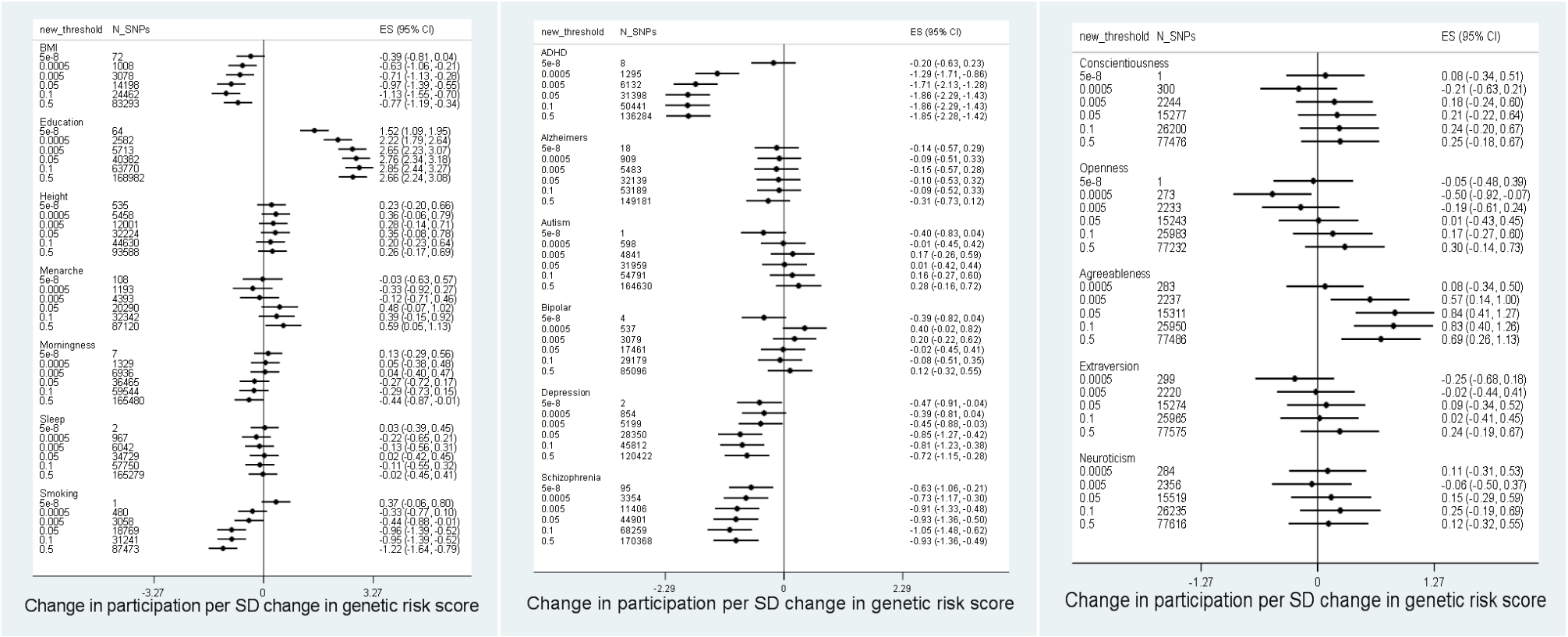






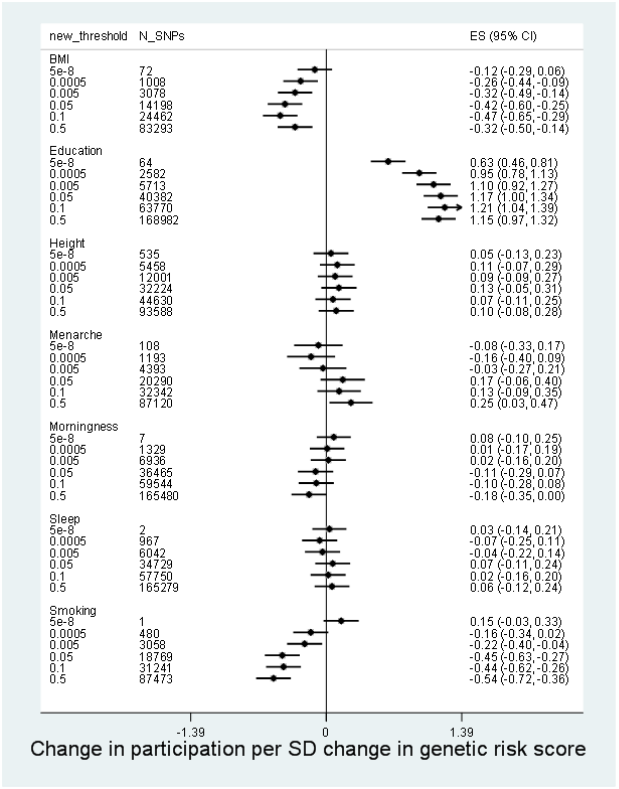
Age at menarche analysis only in females

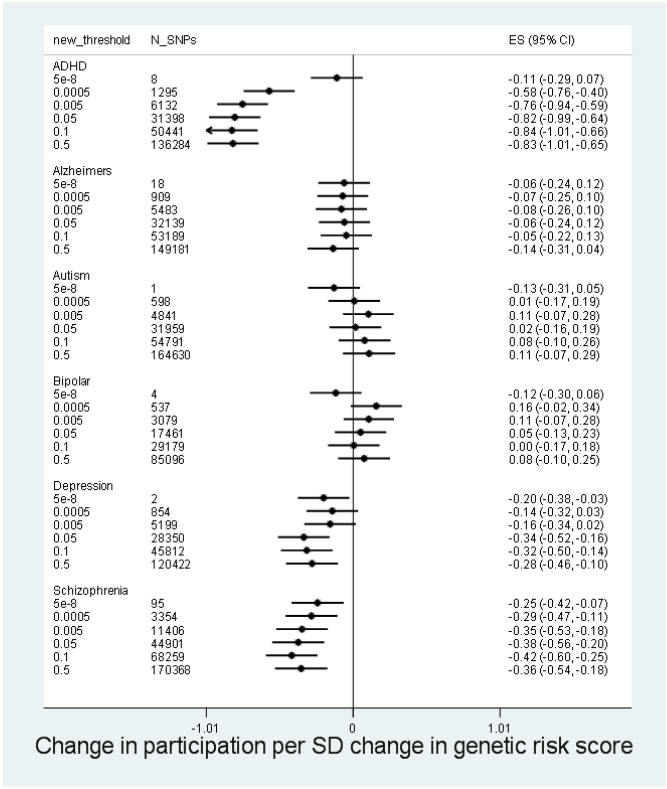
Figure S7. Associations between polygenic risk scores and total questionnaire completion in ALSPAC children (N=7,508)

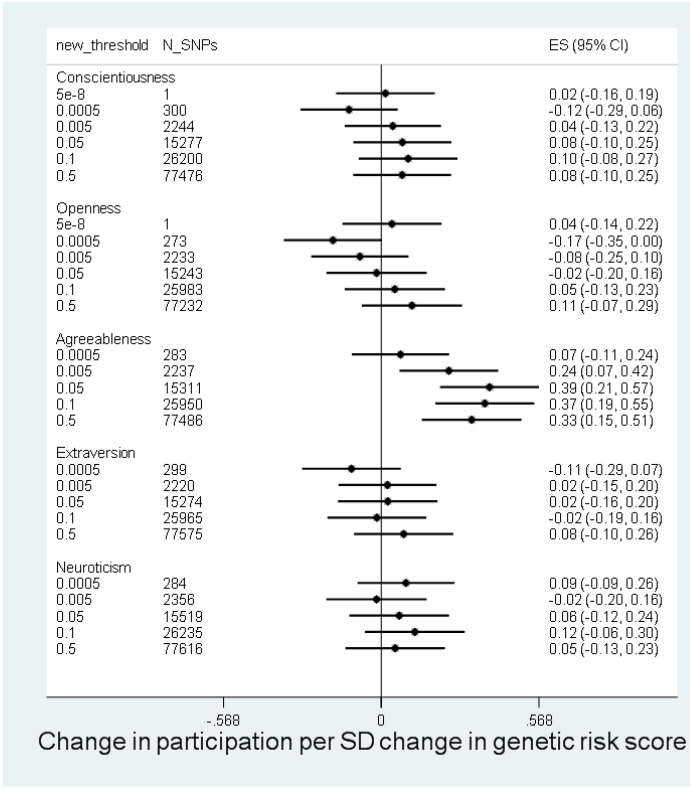


Age at menarche analysis only in females

Figure S8. . Associations between polygenic risk scores and child completed questionnnaires in ALSPAC children (N=7,508)







Age at menarche analysis only in females

Figure S9. . Associations between polygenic risk scores and total number of clinics attended in ALSPAC children (N=7,508)

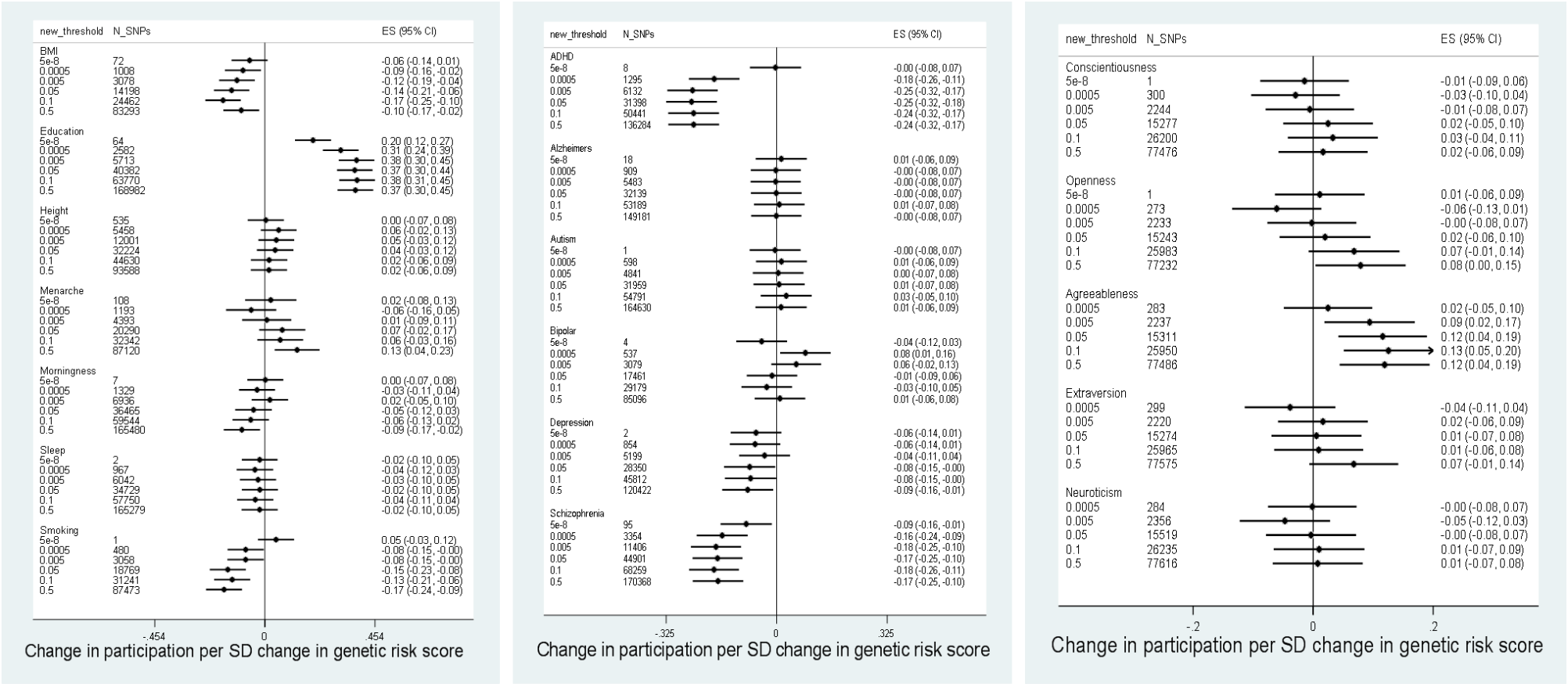
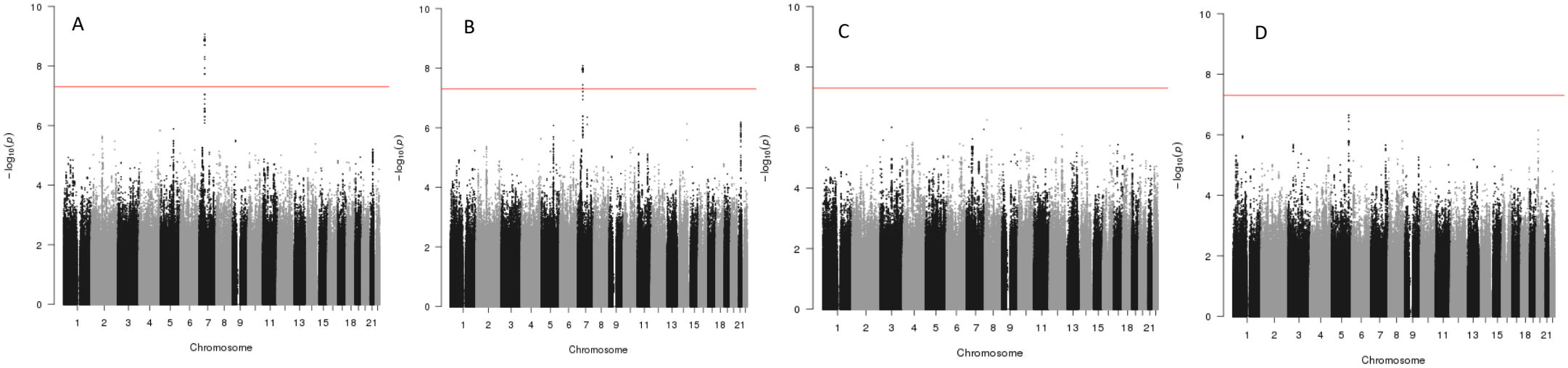
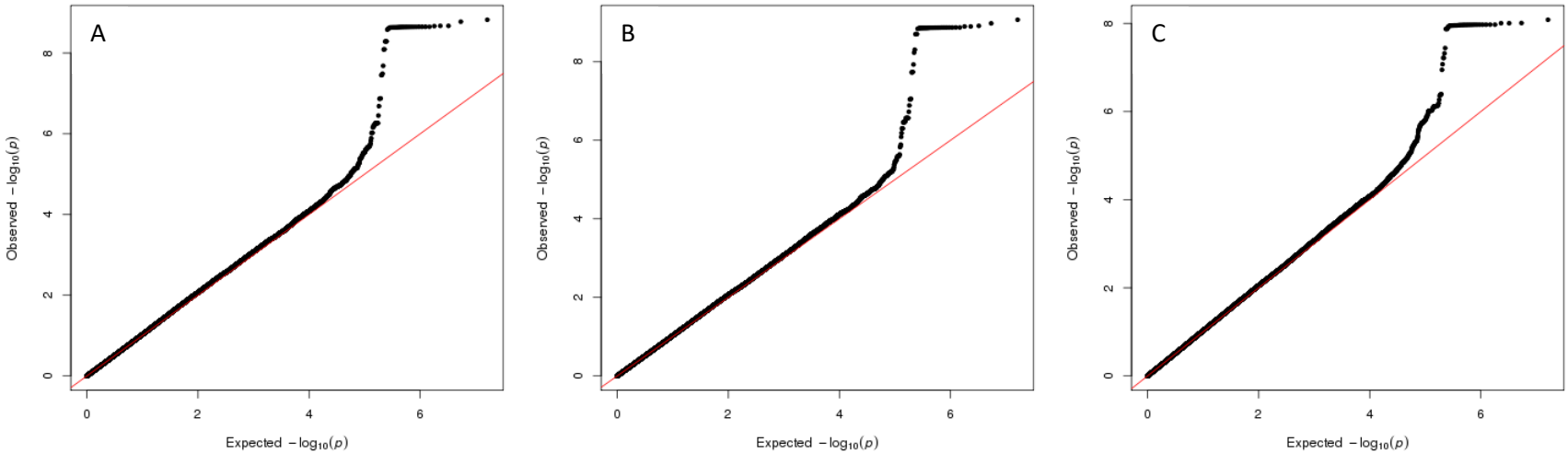


Figure S10. Manhattan plots for GWAS of mother last clinic and mother last questionnaire



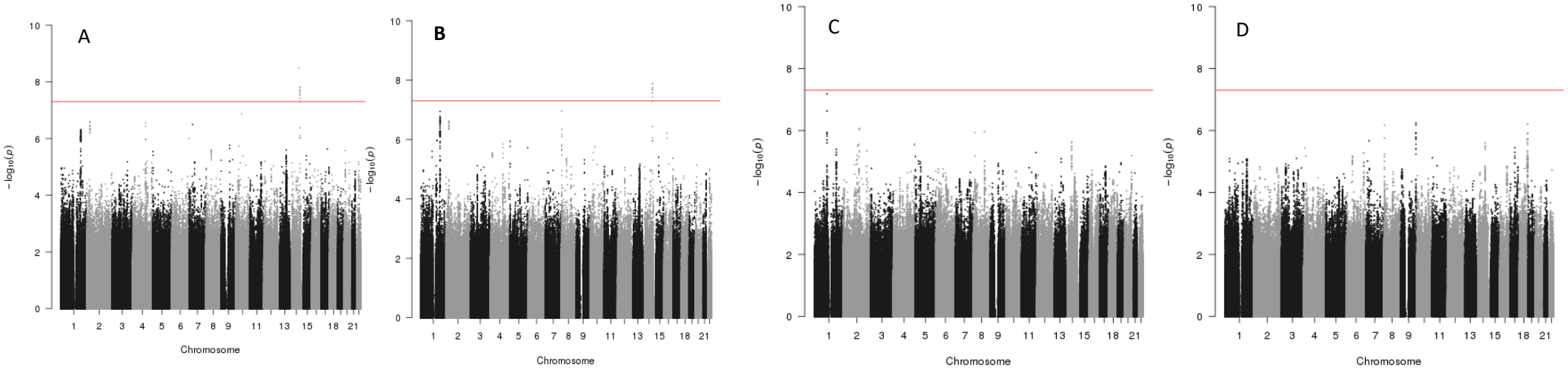
A) Mother total questionnaire, B) Mother questionnaire, C) Mother last clinic, D) Mother last questionnaire

Figure S11. QQ plots for GWAS of total participation, total questionnaire and mother questionnaire in the ALSPAC mothers



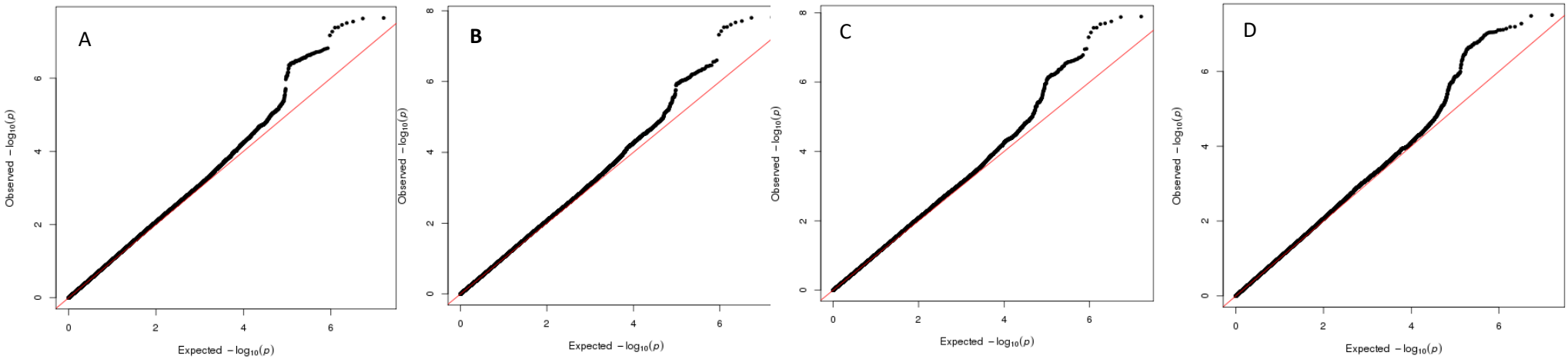
A) Total participation, B) Total questionnaire, C) Mother questionnaire

Figure S12. Manhattan plots for GWAS of participation in children



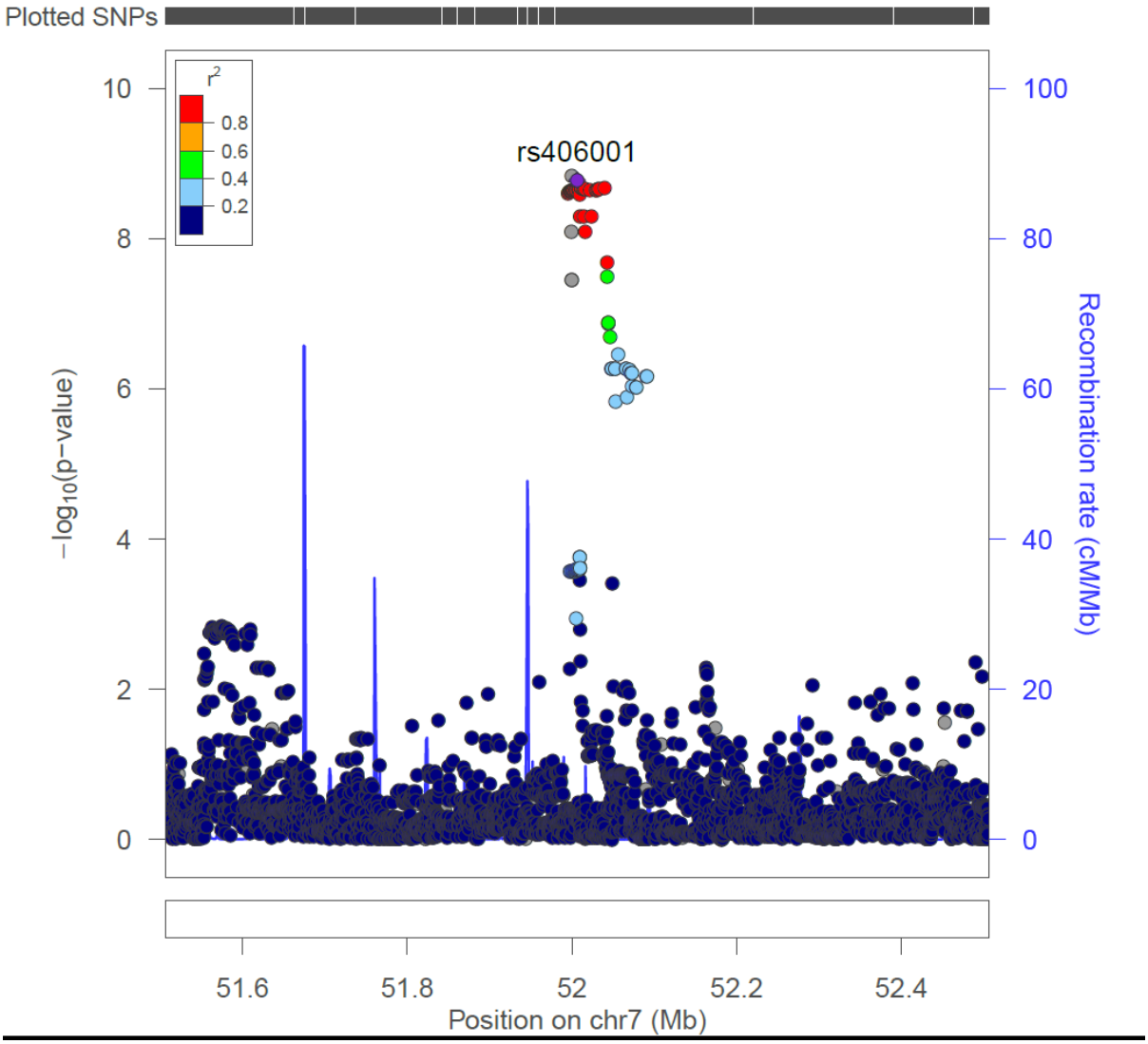
A) Total questionnaire, B) Child questionnaire, C) Child last questionnaire, D) Child last clinic

Figure S13. QQ plots for GWAS of total participation, total questionnaire and mother questionnaire in the ALSPAC mothers



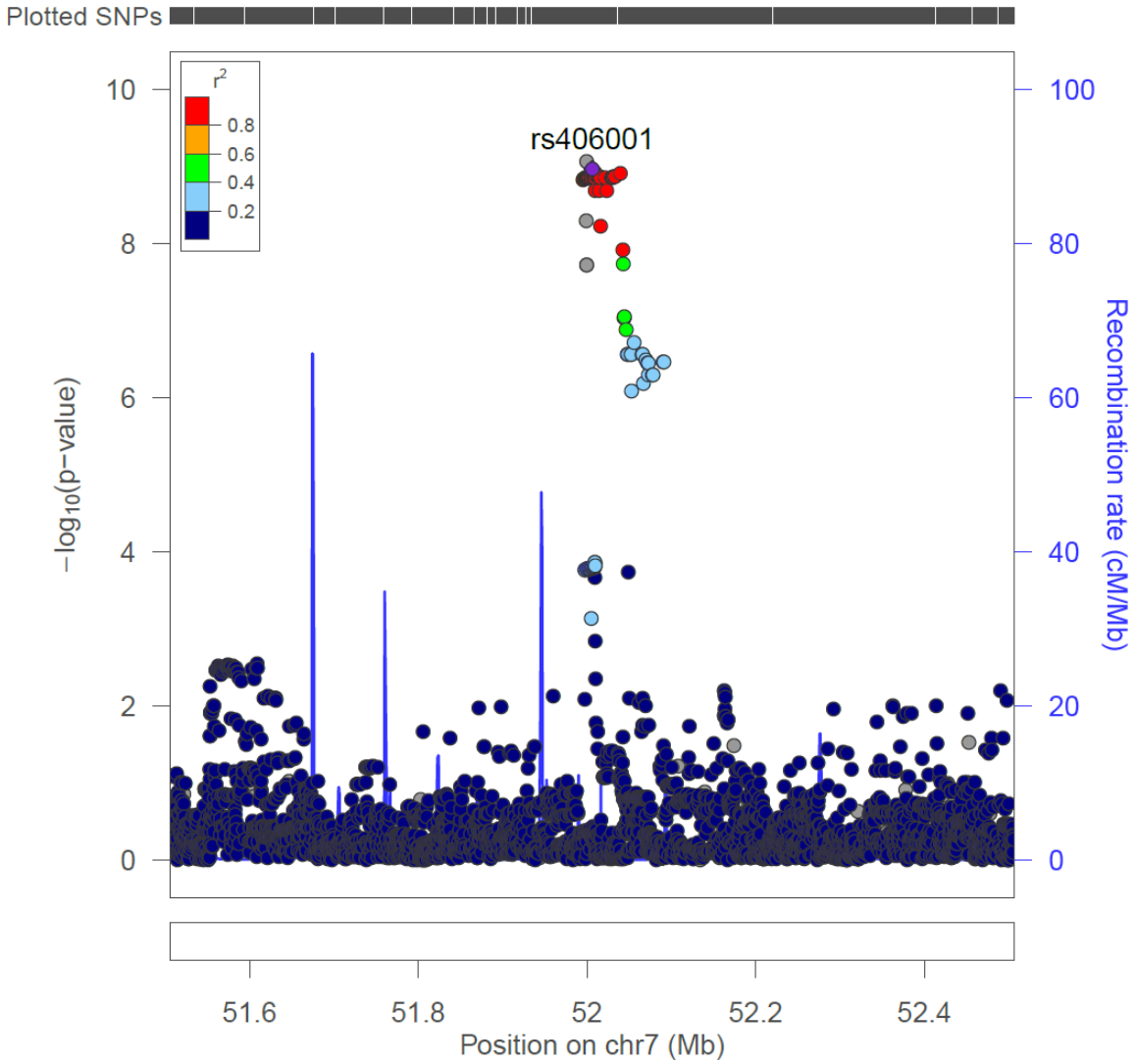
A) Total participation, B) Total questionnaire C) Child questionnaire, D) Child clinic

Figure S14. Regional plot of genomewide significant locus for mother total participation



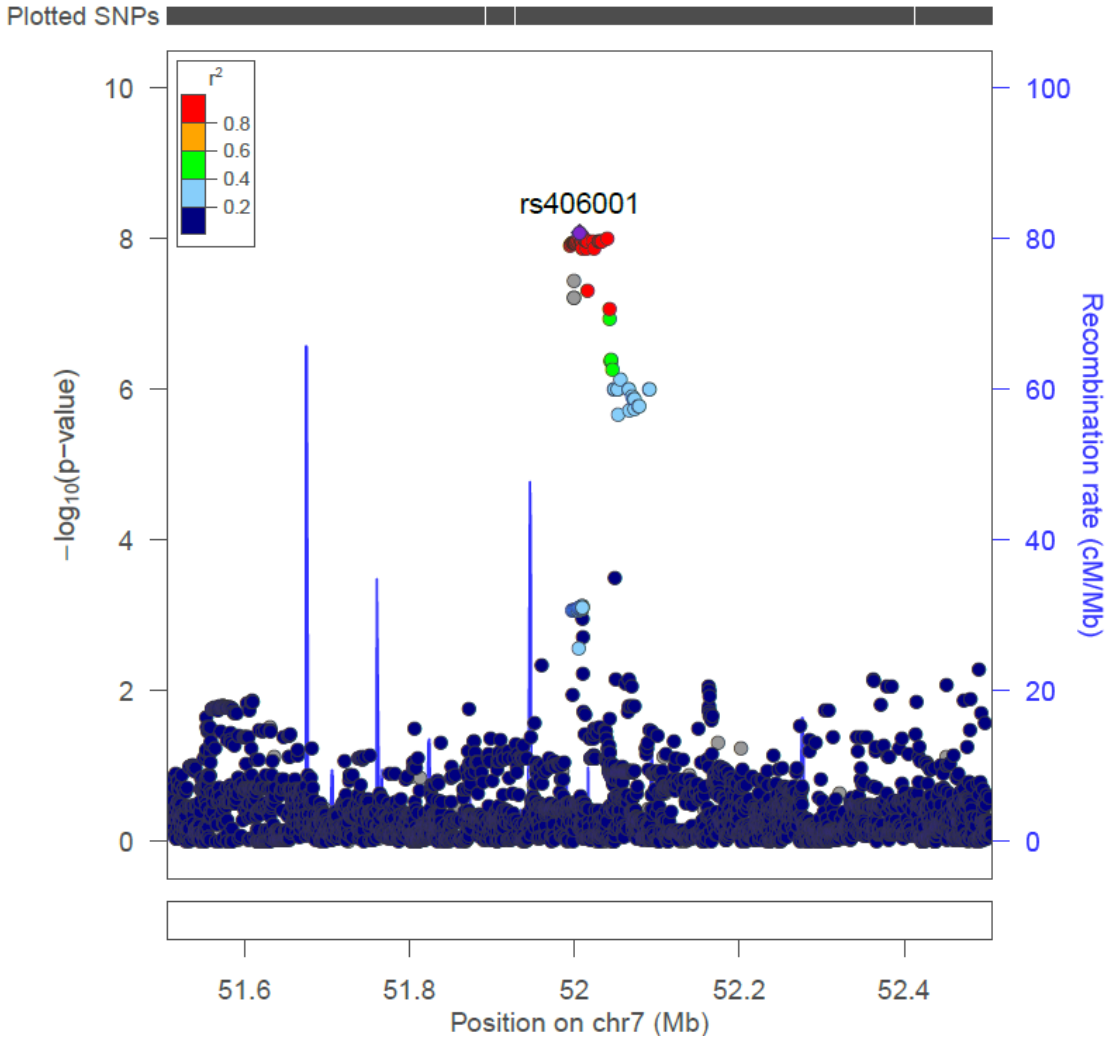
The SNP with the second smallest p-value was used as LD information was not available for the top SNP. The top SNP in each region is highlighted in purple and the surrounding SNPs are colour coded to reflect their LD with this variant. Estimated recombination rates are plotted in blue to reflect local LD structure. Regional plots generated using Locus Zoom, Genome build= hg19.

Figure S15. Regional plot of genomewide significant locus for mother total questionnaire



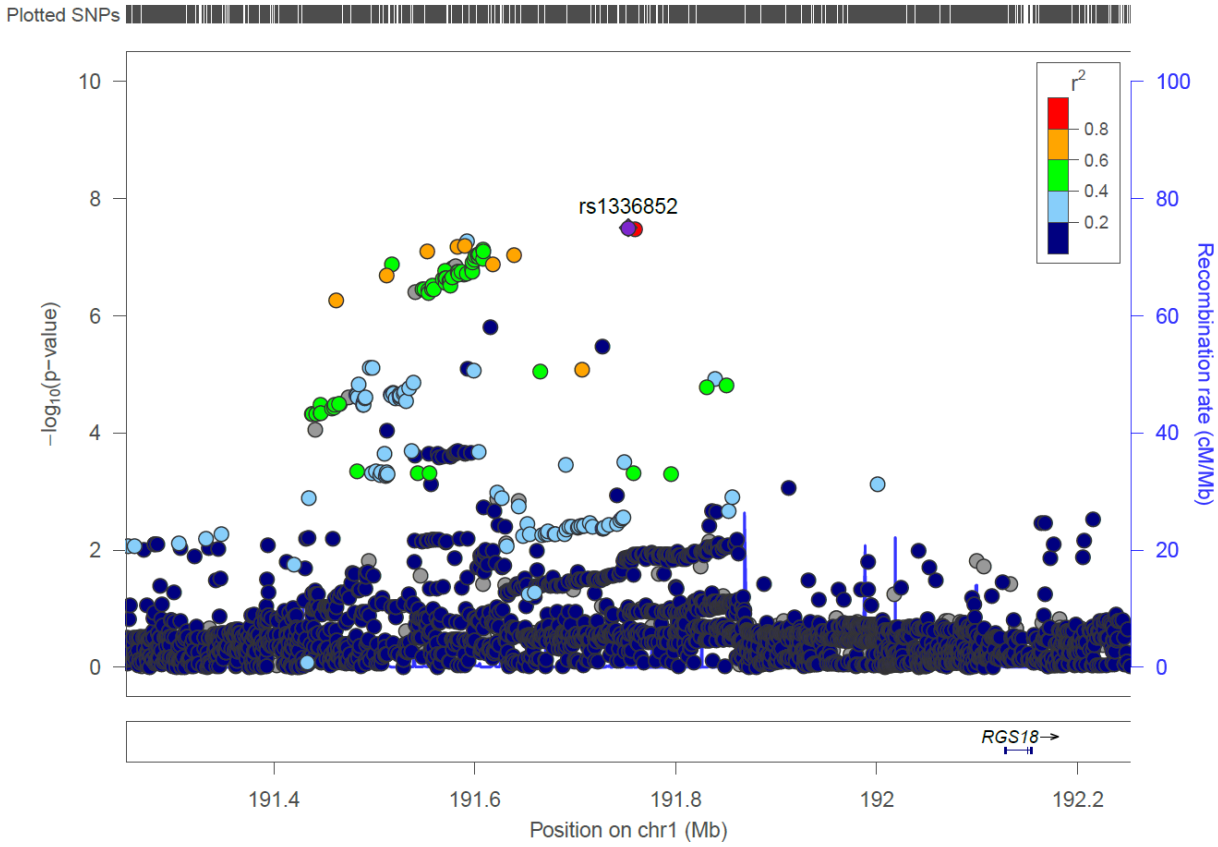
The SNP with the second smallest p-value was used as LD information was not available for the top SNP. The top SNP in each region is highlighted in purple and the surrounding SNPs are colour coded to reflect their LD with this variant. Estimated recombination rates are plotted in blue to reflect local LD structure. Regional plots generated using Locus Zoom, Genome build= hg19.

Figure S16. Regional plot of genomewide significant locus for mother questionnaire



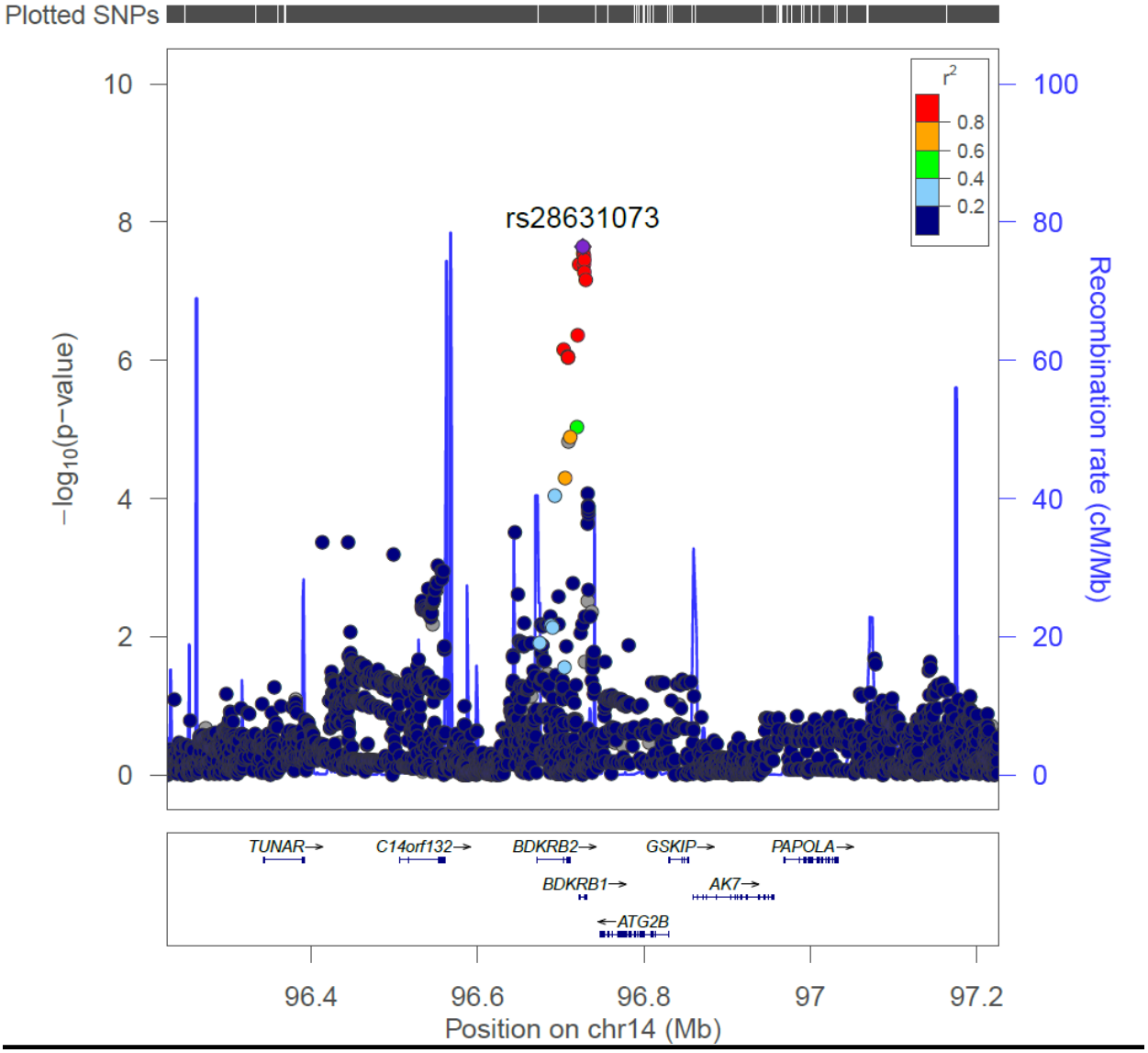
The top SNP in each region is highlighted in purple and the surrounding SNPs are colour coded to reflect their LD with this variant. Estimated recombination rates are plotted in pale blue to reflect local LD structure. Regional plots generated using Locus Zoom, Genome build= hg19.

Figure S17. Regional plot of genomewide significant locus for child clinic attendance



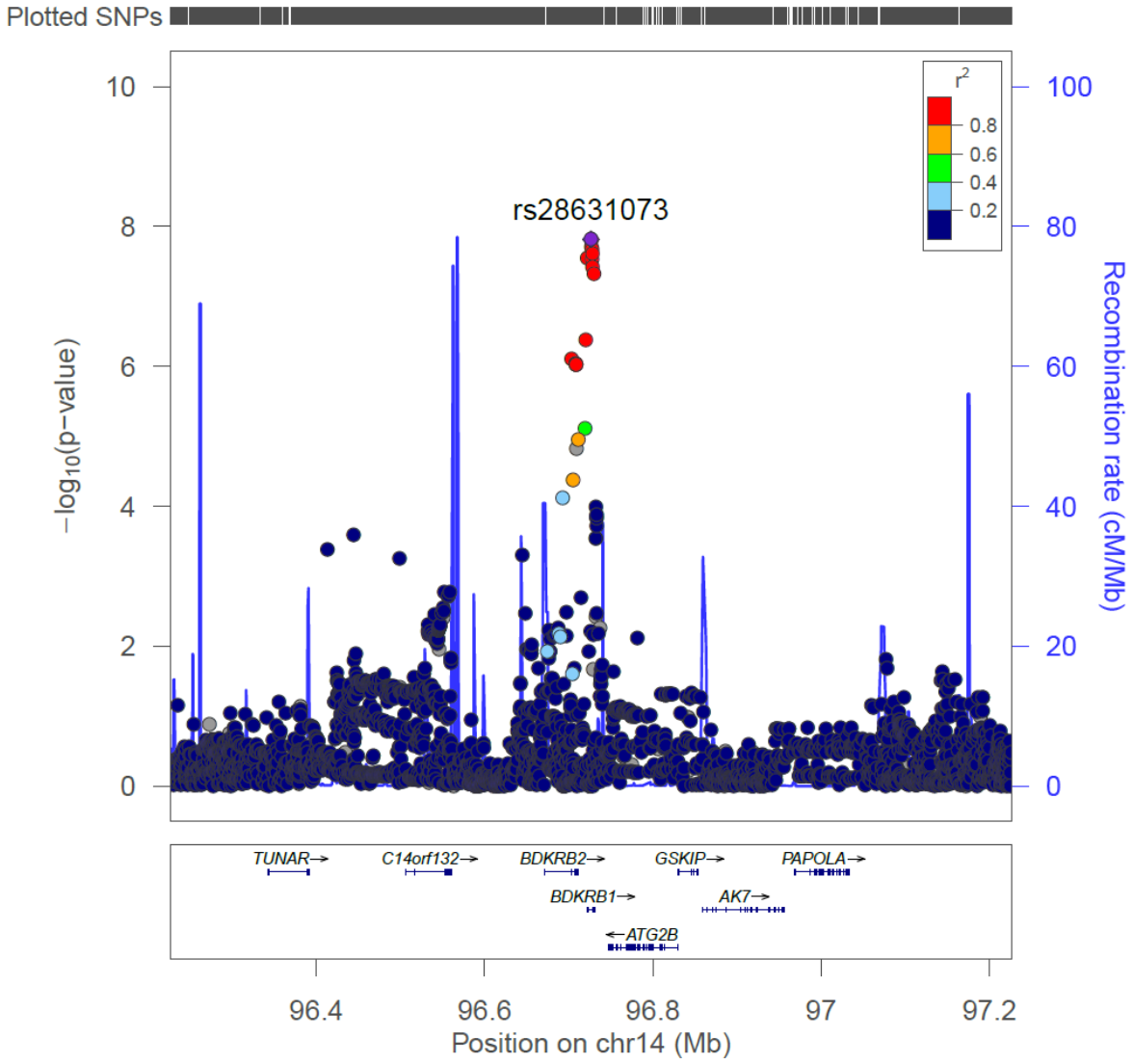
The top SNP in each region is highlighted in purple and the surrounding SNPs are colour coded to reflect their LD with this variant. Estimated recombination rates are plotted in pale blue to reflect local LD structure. Regional plots generated using Locus Zoom, Genome build= hg19.

Figure S18. Regional plot of genomewide significant locus for child total participation



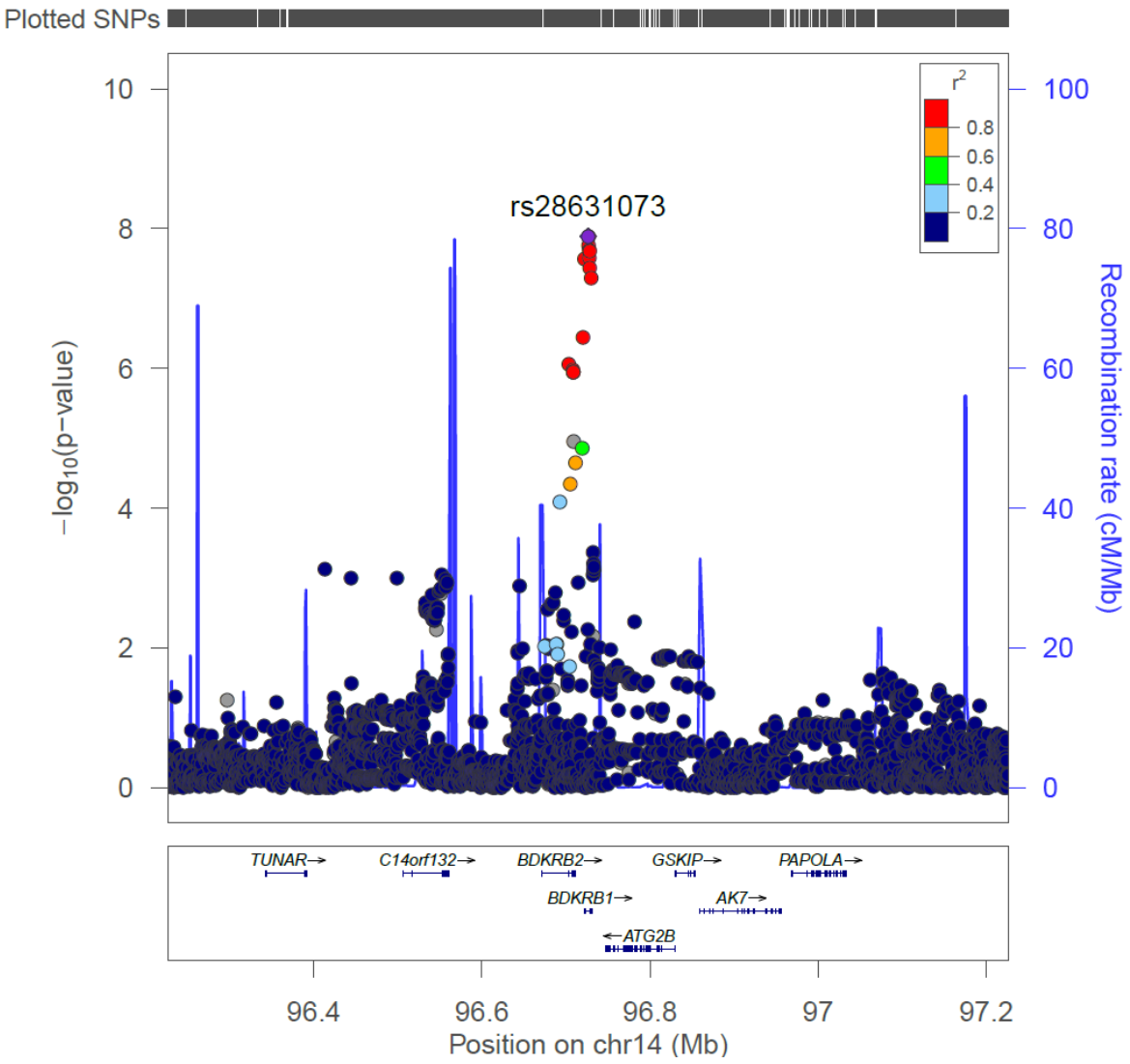
The top SNP in each region is highlighted in purple and the surrounding SNPs are colour coded to reflect their LD with this variant. Estimated recombination rates are plotted in pale blue to reflect local LD structure. Regional plots generated using Locus Zoom, Genome build= hg19.

Figure S19. Regional plot of genomewide significant locus for child total questionnaire



The top SNP in each region is highlighted in purple and the surrounding SNPs are colour coded to reflect their LD with this variant. Estimated recombination rates are plotted in pale blue to reflect local LD structure. Regional plots generated using Locus Zoom, Genome build= hg19.

Figure S20. Regional plot of genomewide significant locus for child questionnaire



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